

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/571,571  
Source: 1Fwp  
Date Processed by STIC: 3/21/06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/591,571</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 <input type="checkbox"/> Use of <220>	Sequence(s) <input type="checkbox"/> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" <b>can only</b> represent a single <u>nucleotide</u> ; "Xaa" <b>can only</b> represent a single <u>amino acid</u>	



IFWP

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006  
TIME: 14:09:12

Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

3 <110> APPLICANT: HuBit Genomix, Inc.  
4 Doi, Toshio  
6 <120> TITLE OF INVENTION: A method for detecting diabetic nephropathy and kits  
7 therefor, agents for preventing and/or treating  
8 diabetic nephropathy, a method for identifying  
9 substances effective in prevention and/or treatment  
10 and kits therefor  
12 <130> FILE REFERENCE: FP-039PCT  
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/571,511  
C--> 15 <141> CURRENT FILING DATE: 2006-03-10  
17 <150> PRIOR APPLICATION NUMBER: JP P2003-319538  
18 <151> PRIOR FILING DATE: 2003-09-11  
20 <160> NUMBER OF SEQ ID NOS: 24  
22 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

*This is not an RNA sequence*

24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 1990  
E--> 26 <212> TYPE: mRNA *invalid response.* Does Not Comply  
27 <213> ORGANISM: Homo sapiens *Per sequence rules, the* Corrected Diskette Needed  
29 <220> FEATURE:  
30 <221> NAME/KEY: CDS  
31 <222> LOCATION: (433)..(1830)  
33 <400> SEQUENCE: 1  
34 gaattccggg ggtattggca gctgaggagt ggaggctggg cagctccgac tccctgacgc 60  
36 cagcgcgacc agatcaatcc aggtccagg agaaagcagg cgggcggcgg gagaaggag 120  
38 aggccgagcg gctcaaccccg gcccggaggct cggggagcgg agagtggcgc accggccggc 180  
40 cgtccggacc cggccgcga gaccccgctc gcccggccac tcgtgtccc gcacggacgg 240  
42 gcgccgcgc aacccgggtgc tgactgggtt actttttaa acactaggaa tggtaatttc 300  
44 tactcttctg gacttcaaac taagaagtta aagagacttc tctgtaaata aacaaatctc 360  
46 ttctgtgtc ctttgtcatt tggagacagc tttatccatcatatccaaag gagtataact 420  
48 agtgctgtca tt atg aat gtg aca agt tta ttt tcc ttt aca agt cca gct 471  
49 Met Asn Val Thr Ser Leu Phe Ser Phe Thr Ser Pro Ala  
50 1 5 10  
52 gtg aag aga ctt ctt ggg tgg aaa cag ggc gat gaa gaa gaa aaa tgg 519  
53 Val Lys Arg Leu Leu Gly Trp Lys Gln Gly Asp Glu Glu Lys Trp  
54 15 20 25  
56 gca gag aaa gct gtt gat gct ttg gtg aaa aaa ctg aag aaa aag aaa 567  
57 Ala Glu Lys Ala Val Asp Ala Leu Val Lys Lys Leu Lys Lys Lys  
58 30 35 40 45  
60 ggt gcc atg gag gaa aag gcc ttg agc tgc cca ggg caa ccg 615  
*Explain any modifications in*  
*modifications in*  
*2207-2237 section (on*  
*2237 line)*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/571,511

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Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

61	Gly	Ala	Met	Glu	Glu	Leu	Glu	Lys	Ala	Leu	Ser	Cys	Pro	Gly	Gln	Pro	
62			50			55								60			
64	agt	aac	tgt	gtc	acc	att	ccc	cgc	tct	ctg	gat	ggc	agg	ctg	caa	gtc	663
65	Ser	Asn	Cys	Val	Thr	Ile	Pro	Arg	Ser	Leu	Asp	Gly	Arg	Leu	Gln	Val	
66			65			70								75			
68	tcc	cac	cgg	aag	gga	ctg	cct	cat	gtc	att	tac	tgc	cgt	gtg	tgg	cgc	711
69	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr	Cys	Arg	Val	Trp	Arg	
70			80			85							90				
72	tgg	ccc	gat	ctt	cag	agc	cac	cat	gaa	cta	aaa	cca	ctg	gaa	tgc	tgt	759
73	Trp	Pro	Asp	Leu	Gln	Ser	His	His	Glu	Leu	Lys	Pro	Leu	Glu	Cys	Cys	
74			95			100							105				
76	gag	ttt	cct	ttt	ggt	tcc	aag	cag	aag	gag	gtc	tgc	atc	aat	ccc	tac	807
77	Glu	Phe	Pro	Phe	Gly	Ser	Lys	Gln	Lys	Glu	Val	Cys	Ile	Asn	Pro	Tyr	
78	110			115			120						125				
80	cac	tat	aag	aga	gta	gaa	agc	cct	gta	ctt	cct	gtg	ctg	gtt	cca	855	
81	His	Tyr	Lys	Arg	Val	Glu	Ser	Pro	Val	Leu	Pro	Pro	Val	Leu	Val	Pro	
82			130			135							140				
84	aga	cac	agc	gaa	tat	aat	cct	cag	cac	agc	ctc	tta	gct	cag	ttc	cgt	903
85	Arg	His	Ser	Glu	Tyr	Asn	Pro	Gln	His	Ser	Leu	Leu	Ala	Gln	Phe	Arg	
86			145			150							155				
88	aac	tta	gga	caa	aat	gag	cct	cac	atg	cca	ctc	aac	gcc	act	ttt	cca	951
89	Asn	Leu	Gly	Gln	Asn	Glu	Pro	His	Met	Pro	Leu	Asn	Ala	Thr	Phe	Pro	
90			160			165							170				
92	gat	tct	ttc	cag	caa	ccc	aac	agc	cac	ccg	ttt	cct	cac	tct	ccc	aat	999
93	Asp	Ser	Phe	Gln	Gln	Pro	Asn	Ser	His	Pro	Phe	Pro	His	Ser	Pro	Asn	
94			175			180							185				
96	agc	agt	tac	cca	aac	tct	ggg	agc	agc	agc	agc	acc	tac	cct	cac	1047	
97	Ser	Ser	Tyr	Pro	Asn	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Thr	Tyr	Pro	His	
98	190			195			200						205				
100	tct	ccc	acc	agc	tca	gac	cca	gga	agc	cct	ttc	cag	atg	cca	gct	gat	1095
101	Ser	Pro	Thr	Ser	Ser	Asp	Pro	Gly	Ser	Pro	Phe	Gln	Met	Pro	Ala	Asp	
102			210			215							220				
104	acg	ccc	cca	cct	gct	tac	ctg	cct	gaa	gac	ccc	atg	acc	cag	gat	1143	
105	Thr	Pro	Pro	Pro	Ala	Tyr	Leu	Pro	Pro	Glu	Asp	Pro	Met	Thr	Gln	Asp	
106			225			230							235				
108	ggc	tct	cag	ccg	atg	gac	aca	aac	atg	atg	gct	ccc	ctg	ccc	tca	1191	
109	Gly	Ser	Gln	Pro	Met	Asp	Thr	Asn	Met	Met	Ala	Pro	Pro	Leu	Pro	Ser	
110			240			245							250				
112	gaa	atc	aac	aga	gga	gat	gtt	cag	gct	ttt	gat	tat	gag	gaa	cca	aaa	1239
113	Glu	Ile	Asn	Arg	Gly	Asp	Val	Gln	Ala	Val	Ala	Tyr	Glu	Glu	Pro	Lys	
114			255			260							265				
116	cac	tgg	tgc	tct	att	gtc	tac	tat	gag	ctc	aac	aat	cgt	gtg	ggt	gaa	1287
117	His	Trp	Cys	Ser	Ile	Val	Tyr	Tyr	Glu	Leu	Asn	Asn	Arg	Val	Gly	Glu	
118	270			275			280						285				
120	gcg	ttc	cat	gcc	tcc	tcc	aca	agt	gtg	ttt	gtt	gat	ggt	ttc	act	gat	1335
121	Ala	Phe	His	Ala	Ser	Ser	Thr	Ser	Val	Leu	Val	Asp	Gly	Phe	Thr	Asp	
122			290			295							300				
124	cct	tcc	aac	aat	aag	aac	cgt	ttc	tgc	ttt	ggg	ctg	ctc	tcc	aat	gtt	1383
125	Pro	Ser	Asn	Asn	Lys	Asn	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	

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126	305	310	315													
128 aac	cggtt	act	att	gaa aac acc agg	cggtt	cat	att	gga	aaa	gga	1431					
129 Asn	Arg	Asn	Ser	Thr	Ile	Glu	Asn	Thr	Arg	Arg	His	Ile	Gly	Lys	Gly	
130	320						325				330					
132 gtt	cat	ctt	tat	tat	gtt	gga	ggg	gag	gtg	tat	gcc	gaa	tgc	ctt	agt	1479
133 Val	His	Leu	Tyr	Tyr	Val	Gly	Gly	Glu	Val	Tyr	Ala	Glu	Cys	Leu	Ser	
134	335						340				345					
136 gac	agt	agc	atc	ttt	gtt	caa	agt	cggtt	aac	tgc	aac	tac	cat	cat	gga	1527
137 Asp	Ser	Ser	Ile	Phe	Val	Gln	Ser	Arg	Asn	Cys	Asn	Tyr	His	His	Gly	
138 350							355				360			365		
140 ttt	cat	cct	act	act	gtt	tgc	aag	atc	cct	agt	ggg	tgt	agt	ctg	aaa	1575
141 Phe	His	Pro	Thr	Thr	Val	Cys	Lys	Ile	Pro	Ser	Gly	Cys	Ser	Leu	Lys	
142	370						375				380					
144 att	ttt	aac	aac	caa	gaa	ttt	gct	cag	tta	ttg	gca	cag	tct	gtg	aac	1623
145 Ile	Phe	Asn	Asn	Gln	Glu	Phe	Ala	Gln	Leu	Leu	Ala	Gln	Ser	Val	Asn	
146	385						390				395					
148 cat	gga	ttt	gag	aca	gtc	tat	gag	ctt	aca	aaa	atg	tgt	act	ata	cgt	1671
149 His	Gly	Phe	Glu	Thr	Val	Tyr	Glu	Leu	Thr	Lys	Met	Cys	Thr	Ile	Arg	
150	400						405				410					
152 atg	agc	ttt	gtt	aag	ggc	tgg	gga	gca	gaa	tac	cac	cgc	cag	gat	gtt	1719
153 Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Ala	Glu	Tyr	His	Arg	Gln	Asp	Val	
154	415						420				425					
156 act	agc	acc	ccc	tgc	tgg	att	gag	ata	cat	ctg	cac	ggc	ccc	ctc	cag	1767
157 Thr	Ser	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His	Leu	His	Gly	Pro	Leu	Gln	
158 430							435				440			445		
160 tgg	ctg	gat	aaa	gtt	ctt	act	caa	atg	ggt	tca	cct	cat	aat	cct	att	1815
161 Trp	Leu	Asp	Lys	Val	Leu	Thr	Gln	Met	Gly	Ser	Pro	His	Asn	Pro	Ile	
162	450						455				460					
164 tca	tct	gta	tct	taa	atggcccgag	catctgcctc	ttggaaaaacta	tttgaggcttg								1870
165 Ser	Ser	Val	Ser													
166	465															
168 catgtacttg	aaaggatggat	gagtcagacaca	cgattgagaa	ctgacaaagg	agccttgata											1930
170 atacttgacc	tgtgtgacca	actgttggat	tcagaaaattt	aaacaaaaaaa	aaaaaaaaaa											1990
173 <210>	SEQ ID NO:	2														
174 <211>	LENGTH:	1970														
E--> 175 <212>	TYPE:	mRNA	same exon													
176 <213>	ORGANISM:	Homo sapiens														
178 <220>	FEATURE:															
179 <221>	NAME/KEY:	CDS														
180 <222>	LOCATION:	(283) .. (1794)														
182 <400>	SEQUENCE:	2														
183 agggaaacggt	ttattaggag	ggagtggtgg	agctgggcca	ggcagggaaaga	cgctggaaata	60										
185 agaaaacattt	ttgctccagc	ccccatccca	gtcccccggag	gctgcccgcgc	cagctgcgc	120										
187 gagcgagccc	ctccccggct	ccagccccgg	ccggggccgc	gcccggacccc	agccccgcgt	180										
189 ccagcgctgg	cggtgcaact	gccccccgcgc	ggtggaggggg	agggtggccccc	ggtccgcgcga	240										
191 aggctagcgc	cccgccacccc	gcagagcggg	cccagaggga	cc	atg	acc	ttg	ggc								294
192																
193															1	
195 tcc	ccc	agg	aaa	ggc	ctt	ctg	atg	ctg	atg	gcc	ttg	gtg	acc	cag		342

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/571,511

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Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

196	Ser	Pro	Arg	Lys	Gly	Leu	Leu	Met	Leu	Leu	Met	Ala	Leu	Val	Thr	Gln	
197	5					10					15				20		
199	gga	gac	cct	gtg	aag	ccg	tct	cg	ggc	ccg	ctg	gtg	acc	tgc	acg	tgt	390
200	Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro	Leu	Val	Thr	Cys	Thr	Cys	
201						25					30				35		
203	gag	agc	cca	cat	tgc	aag	ggg	cct	acc	tgc	cg	ggg	gcc	tgg	tgc	aca	438
204	Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr	Cys	Arg	Gly	Ala	Trp	Cys	Thr	
205						40					45				50		
207	gta	gtg	ctg	gtg	cg	gag	ggg	agg	cac	ccc	cag	gaa	cat	cgg	ggc		486
208	Val	Val	Leu	Val	Arg	Glu	Glu	Gly	Arg	His	Pro	Gln	Glu	His	Arg	Gly	
209						55					60				65		
211	tgc	ggg	aac	ttg	cac	agg	gag	ctc	tgc	agg	ggg	cg	ccc	acc	gag	ttc	534
212	Cys	Gly	Asn	Leu	His	Arg	Glu	Leu	Cys	Arg	Gly	Arg	Pro	Thr	Glu	Phe	
213						70					75				80		
215	gtc	aa	cac	tac	tgc	tgc	gac	agc	cac	ctc	tgc	aa	cac	aa	gt	tcc	582
216	Val	Asn	His	Tyr	Cys	Cys	Asp	Ser	His	Leu	Cys	Arg	Gly	Arg	Pro	Thr	
217						85					90				95		100
219	ctg	gtg	ctg	gag	ggc	acc	caa	cct	cct	tcg	gag	cag	ccg	gga	aca	gat	630
220	Leu	Val	Leu	Glu	Ala	Thr	Gln	Pro	Pro	Ser	Glu	Gln	Pro	Gly	Thr	Asp	
221						105					110				115		
223	ggc	cag	ctg	ggc	ctg	atc	ctg	ggc	ccc	gtg	ctg	ggc	ttg	ctg	ggc	ctg	678
224	Gly	Gln	Leu	Ala	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu	Leu	Ala	Leu	
225						120					125				130		
227	gtg	ggc	ctg	ggt	gtc	ctg	ggc	ctg	tgg	cat	gtc	cga	cg	agg	cag	gag	726
228	Val	Ala	Leu	Gly	Val	Leu	Gly	Leu	Trp	His	Val	Arg	Arg	Arg	Gln	Glu	
229						135					140				145		
231	aag	cag	cgt	ggc	ctg	cac	agc	gag	ctg	gga	gag	tcc	agt	ctc	atc	ctg	774
232	Lys	Gln	Arg	Gly	Leu	His	Ser	Glu	Leu	Gly	Glu	Ser	Ser	Leu	Ile	Leu	
233						150					155				160		
235	aaa	gca	tct	gag	cag	ggc	gac	acg	atg	ttg	ggg	gac	ctc	ctg	gac	agt	822
236	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
237						165					170				175		180
239	gac	tgc	acc	aca	ggg	agt	ggc	tca	ggg	ctc	ccc	ttc	ctg	gtg	cag	agg	870
240	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Ile	Pro	Phe	Leu	Val	Gln	Arg	
241						185					190				195		
243	aca	gtg	gca	cg	cag	gtt	ggc	ttg	gtg	gag	tgt	gtg	gga	aaa	ggc	cg	918
244	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	
245						200					205				210		
247	tat	ggc	gaa	gtg	tgg	cg	ggc	ttg	tgg	cac	gg	gt	gt	gg	gt	gt	966
248	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val	
249						215					220				225		
251	aag	atc	tcc	tcc	tcg	agg	gat	gaa	cag	tcc	tgg	ttc	cg	gg	act	gag	1014
252	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu	
253						230					235				240		
255	atc	tat	aa	aca	gta	ttg	ctc	aga	cac	gac	aa	atc	cta	ggc	ttc	atc	1062
256	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile	
257						245					250				255		260
259	gcc	tca	gac	atg	acc	tcc	cg	aac	tcg	agc	acg	cag	ctg	tgg	ctc	atc	1110
260	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	

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261	265	270	275	
263 acg cac tac cac gag cac ggc tcc ctc tac gac ttt ctg cag aga cag				1158
264 Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln				
265 280	285	290		
267 acg ctg gag ccc cat ctg gct ctg agg cta gct gtg tcc gcg gca tgc				1206
268 Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys				
269 295	300	305		
271 ggc ctg gcg cac ctg cac gtg gag atc ttc ggt aca cag ggc aaa cca				1254
272 Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro				
273 310	315	320		
275 gcc att gcc cac cgc gac ttc aag agc cgc aat gtg ctg gtc aag agc				1302
276 Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser				
277 325	330	335	340	
279 aac ctg cag tgt tgc atc gcc gac ctg ggc ctg gct gtg atg cac tca				1350
280 Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser				
281 345	350	355		
283 cag ggc agc gat tac ctg gac atc ggc aac aac ccg aga gtg ggc acc				1398
284 Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr				
285 360	365	370		
287 aag cgg tac atg gca ccc gag gtg ctg gac gag cag atc cgc acg gac				1446
288 Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp				
289 375	380	385		
291 tgc ttt gag tcc tac aag tgg act gac atc tgg gcc ttt ggc ctg gtg				1494
292 Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val				
293 390	395	400		
295 ctg tgg gag att gcc cgc cgg acc atc gtg aat ggc atc gtg gag gac				1542
296 Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp				
297 405	410	415	420	
299 tat aga cca ccc ttc tat gat gtg gtg ccc aat gac ccc agc ttt gag				1590
300 Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu				
301 425	430	435		
303 gac atg aag aag gtg gtg tgt gtg gat cag cag acc ccc acc atc cct				1638
304 Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro				
305 440	445	450		
307 aac cgg ctg gct gca gac ccg gtc ctc tca ggc cta gct cag atg atg				1686
308 Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met				
309 455	460	465		
311 cgg gag tgc tgg tac cca aac ccc tct gcc cga ctc acc gcg ctg cgg				1734
312 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg				
313 470	475	480		
315 atc aag aag aca cta caa aaa att agc aac agt cca gag aag cct aaa				1782
316 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys				
317 485	490	495	500	
319 gtg att caa tag cccaggagca cctgattcct ttctgcctgc agggggctgg				1834
320 Val Ile Gln				
322 ggggggtgggg ggcagtggat ggtgcctat ctgggttagag gtatgtgag tgtgggtgtgt				1894
324 gctggggatg ggcagctgcg cctgcctgct cggccccag cccacccagc caaaaataca				1954
326 gctgggctga aacctg				1970
329 <210> SEQ ID NO: 3				

RAW SEQUENCE LISTING  
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Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

330 <211> LENGTH: 1547  
**E--> 331 <212> TYPE: mRNA** *None*  
 332 <213> ORGANISM: Homo sapiens  
 334 <220> FEATURE:  
 335 <221> NAME/KEY: CDS  
 336 <222> LOCATION: (324)..(1514)  
 338 <400> SEQUENCE: 3  
 339 ggggacttct tgaacttgca gggagaataa cttgcgcacc ccactttgcg ccgggtgcctt 60  
 341 tgcccccagcg gagcctgctt cgccatctcc gagccccacc gcccctccac tcctcggcct 120  
 343 tgcccgacac tgagacgctg ttcccagcgt gaaaagagag actgcgcggc cggcacccgg 180  
 345 gagaaggagg aggcaaagaa aaggaacgga cattcggtcc ttgcgcagg tccttgacc 240  
 347 agagtttttc catgtggacg ctctttcaat ggacgtgtcc cgcgtgctt cttagacgga 300  
 349 ctgcggtctc ctaaaggctcg acc atg gtg gcc acc cgc tgt ctt cta gcg 353  
 350 Met Val Ala Gly Thr Arg Cys Leu Leu Ala  
 351 1 5 10  
 353 ttg ctg ctt ccc cag gtc ctc ctg ggc ggc gcg gct ggc ctc gtt ccg 401  
 354 Leu Leu Leu Pro Gln Val Leu Leu Gly Gly Ala Ala Gly Leu Val Pro  
 355 15 20 25  
 357 gag ctg ggc cgc agg aag ttc gcg gcg tcg tcg ggc cgc ccc tca 449  
 358 Glu Leu Gly Arg Arg Lys Phe Ala Ala Ser Ser Gly Arg Pro Ser  
 359 30 35 40  
 361 tcc cag ccc tct gac gag gtc ctg agc gag ttc gag ttg cgg ctg ctc 497  
 362 Ser Gln Pro Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu  
 363 45 50 55  
 365 agc atg ttc ggc ctg aaa cag aga ccc acc ccc agc agg gac gcc gtg 545  
 366 Ser Met Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val  
 367 60 65 70  
 369 gtg ccc ccc tac atg cta gac ctg tat cgc agg cac tca ggt cag ccg 593  
 370 Val Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro  
 371 75 80 85 90  
 373 ggc tca ccc gcc cca gac cac cgg ttg gag agg gca gcc agc cga gcc 641  
 374 Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala  
 375 95 100 105  
 377 aac act gtg cgc agc ttc cac cat gaa gaa tct ttg gaa gaa cta cca 689  
 378 Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro  
 379 110 115 120  
 381 gaa acg agt ggg aaa aca acc cgg aga ttc ttc ttt aat tta agt tct 737  
 382 Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser  
 383 125 130 135  
 385 atc ccc acg gag gag ttt atc acc tca gca gag ctt cag gtt ttc cga 785  
 386 Ile Pro Thr Glu Glu Phe Ile Thr Ser Ala Glu Leu Gln Val Phe Arg  
 387 140 145 150  
 389 gaa cag atg caa gat gct tta gga aac aat agc agt ttc cat cac cga 833  
 390 Glu Gln Met Gln Asp Ala Leu Gly Asn Asn Ser Ser Phe His His Arg  
 391 155 160 165 170  
 393 att aat att tat gaa atc ata aaa cct gca aca gcc aac tcg aaa ttc 881  
 394 Ile Asn Ile Tyr Glu Ile Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe  
 395 175 180 185  
 397 ccc gtg acc aga ctt ttg gac acc agg ttg gtg aat cag aat gca agc 929

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E--> 456 <212> TYPE mRNA

457 <213> ORGANISM: HO

459 <220> FEATURE:

460 <221> NAME/KEY

461 <222> LOCATION: (47)

463 <400> SEQUENCE: 4

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Input Set : A:\PTO.TS..txt  
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464	gagggagggg	ccgcccggga	agaggaggag	gaaggaaaaga	aagaaaagcga	gggagggaaa	60
466	gaggaggaag	gaagatgcga	gaaggcagag	gaggagggag	ggagggaaagg	agcgcggagc	120
468	ccggcccgga	agcttagtga	gtgtggcatc	cgactgagg	gacgcgagcc	tgagacgccc	180
470	ctgctgtcc	ggctgagtat	ctagttgtc	tccccatgg	gattccgtc	caagctatct	240
472	cgagcctgca	gcccacagt	ccccggccct	cgcccagggtt	cactgcaacc	gttcagaggt	300
474	ccccaggagc	tgctgctggc	gagcccgcta	ctgcaggac	ctatggagcc	attccgttagt	360
476	gccatcccg	gcaacgcact	gctgcagcctt	ccctgagcct	ttccagcaag	tttgcgtcaag	420
478	attggctgtc	aagaatcatg	gactgttatt	atatgccttg	ttttctgtca	agacacc	477
480	atg att cct	ggt aac cga	atg ctg	atg gtc	gtt tta	tgc caa gtc	525
481	Met Ile Pro	Gly Asn Arg	Met Leu Met	Val Val	Leu Leu	Cys Gln Val	
482	1	5	10	15			
484	ctg cta gga	ggc gcg	agc cat	gct agt	ttg ata	cct gag	573
485	Leu Leu Gly	Gly Ala Ser	His Ala Ser	Leu Ile Pro	Glu Thr Gly	Lys	
486	20	25	30				
488	aaa aaa gtc	gcc gag	att cag	ggc cac	gct gga	ggc cgc	621
489	Lys Lys Val	Ala Glu Ile	Gln Gly His	Ala Gly Gly	Arg Arg Ser	Gly	
490	35	40	45				
492	cag agc cat	gag ctc	ctg cgg	gac ttc	gag gcg	aca ctt	669
493	Gln Ser His	Glu Leu Leu	Arg Asp Phe	Glu Ala Thr	Leu Leu Gln	Met	
494	50	55	60				
496	ttt ggg	ctg cgc	cgc cgc	ccg cag	agt cgc	gtc att ccg	717
497	Phe Gly	Leu Arg Arg	Pro Gln Pro	Ser Lys Ser	Ala Val	Ile Pro	
498	65	70	75	80			
500	gac tac atg	cggtt tac	cggtt cag	tct cag	ggg gag	gag gag gaa	765
501	Asp Tyr Met	Arg Asp Leu	Tyr Arg Leu	Gln Ser Gly	Glu Glu Glu		
502	85	90	95				
504	gag cag atc	cac agc act	ggt ctt	gag tat	cct gag	cgc ccg gcc	813
505	Glu Gln Ile	His Ser Thr	Gly Leu Glu	Tyr Pro Glu	Arg Pro Ala	Ser	
506	100	105	110				
508	cgg gcc aac	acc gtg agg	agc ttc	cac cac	gaa gaa	cat ctg gag	861
509	Arg Ala Asn	Thr Val Arg	Ser Phe His	His Glu His	Leu Glu Asn		
510	115	120	125				
512	atc cca	ggg acc	agt gaa	aac tct	gct ttt	cgt ttc ctc	909
513	Ile Pro	Gly Thr Ser	Glu Asn Ser	Ala Phe Arg	Phe Leu Phe	Asn Leu	
514	130	135	140				
516	agc agc atc	cct gag	aac gag	gcg atc	tcc tct	gca gag	957
517	Ser Ser Ile	Pro Glu Asn	Glu Ala Ile	Ser Ser Ala	Glu Leu	Arg Leu	
518	145	150	155	160			
520	ttc cgg	gag cag	gtg gac	cag ggc	cct gat	tgg gaa	1005
521	Phe Arg Glu	Gln Val Asp	Gln Gly Pro	Asp Trp Glu	Arg Gly Phe	His	
522	165	170	175				
524	cgt ata aac	att tat	gag gtt	atg aag	ccc cca	gca gaa	1053
525	Arg Ile Asn	Ile Tyr Glu	Val Met Lys	Pro Pro Ala	Glu Val	Val Pro	
526	180	185	190				
528	ggg cac	ctc atc	aca cga	cta ctg	gac acg	aga ctg	1101
529	Gly His	Leu Ile	Thr Arg	Leu Asp	Thr Arg	Leu Val His	His Asn
530	195	200	205				
532	gtg aca	cggtgg	gaa act	ttt gat	gtg agc	cct gcg	1149
533	Val Thr Arg	Trp Glu	Thr Phe	Asp Val	Ser Pro	Ala Val Leu	Arg Trp

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Input Set : A:\PTO.TS..txt  
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534	210	215	220														
536	acc	cgg	gag	aag	cag	cca	aac	tat	ggg	cta	gcc	att	gag	gtg	act	cac	1197
537	Thr	Arg	Glu	Lys	Gln	Pro	Asn	Tyr	Gly	Leu	Ala	Ile	Glu	Val	Thr	His	
538	225																240
540	ctc	cat	cag	act	cgg	acc	cac	cag	ggc	cag	cat	gtc	agg	att	agc	cga	1245
541	Leu	His	Gln	Thr	Arg	Thr	His	Gln	Gly	Gln	His	Val	Arg	Ile	Ser	Arg	
542																	255
544	tcg	tta	cct	caa	ggg	agt	ggg	aat	tgg	gcc	cag	ctc	cg	ccc	ctc	ctg	1293
545	Ser	Leu	Pro	Gln	Gly	Ser	Gly	Asn	Trp	Ala	Gln	Leu	Arg	Pro	Leu	Leu	
546																	270
548	gtc	acc	ttt	ggc	cat	gat	ggc	cgg	cat	gcc	ttg	acc	cga	cgc	cgg	1341	
549	Val	Thr	Phe	Gly	His	Asp	Gly	Arg	Gly	His	Ala	Leu	Thr	Arg	Arg	Arg	
550																	285
552	agg	gcc	aag	cgt	agc	cct	aag	cat	cac	tca	cag	cgg	gcc	agg	aag	aag	1389
553	Arg	Ala	Lys	Arg	Ser	Pro	Lys	His	His	Ser	Gln	Arg	Ala	Arg	Lys	Lys	
554																	300
556	aat	aag	aac	tgc	cgg	cgc	cac	tgc	ctc	tat	gtg	gac	ttc	agc	gat	gtg	1437
557	Asn	Lys	Asn	Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	
558																	320
560	ggc	tgg	aat	gac	tgg	att	gtg	gcc	cca	cca	ggc	tac	cag	gcc	ttc	tac	1485
561	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	Phe	Tyr	
562																	335
564	tgc	cat	ggg	gac	tgc	ccc	ttt	cca	ctg	gct	gac	cac	ctc	aac	tca	acc	1533
565	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	Asn	Ser	Thr	
566																	350
568	aac	cat	gcc	att	gtg	cag	acc	ctg	gtc	aat	tct	gtc	aat	tcc	agt	atc	1581
569	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	
570																	365
572	ccc	aaa	gcc	tgt	tgt	gtg	ccc	act	gaa	ctg	agt	gcc	atc	tcc	atg	ctg	1629
573	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	
574																	380
576	tac	ctg	gat	gag	tat	gat	aag	gtg	gta	ctg	aaa	aat	tat	cag	gag	atg	1677
577	Tyr	Leu	Asp	Glu	Tyr	Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	
578																	400
580	gta	gta	gag	gga	tgt	ggg	tgc	cgc	tga	gatcaggcag	tccttgagga						1724
581	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg									
582																	405
584	tagacagata	tacacacccac	acacacacac	cacatacacc	acacacacac	gttcccatcc											1784
586	actcaccac	acactacaca	gactgcttcc	ttatactgg	acttttattt	aaaaaaaaaaa											1844
588	aaaaaaaaaaat	ggaaaaaaatc	cctaaacatt	cacccgtacc	ttatccatgtt	ctttacgtgc											1904
590	aaatgttttg	accatattga	tcatatattt	tgacaaaata	tatccataac	tacgttataaa											1964
592	aaaaaaaaaa	taaaatgagt	cattatccat	aaggt													1999
763	<210>	SEQ ID NO:	19														
764	<211>	LENGTH:	4978														

E--> 765 <212> TYPE: mRNA

766 <213> ORGANISM: Homo sapiens  
768 <220> FEATURE:  
769 <221> NAME/KEY: CDS  
770 <222> LOCATION: (241)..(2553)

RAW SEQUENCE LISTING  
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Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

772 <400> SEQUENCE: 19  
 773 ggtttccgga gctcgccgg cgccagactgg gagggggagc cgggggttcc gacgtcgac 60  
 775 ccgagggAAC aagcccaac cggatcctgg acaggcaccc cggcttggcg ctgtctctcc 120  
 777 ccctcggttc ggagaggccc ttcggcctga gggagcctcg ccccccgtcc ccgcacacg 180  
 779 cgcagccccg gcctctcggc ctctgcccggaa aacacgttg ggacccctga ttttagcagg 240  
 781 atg gcc caa tgg aat cag cta cag cag ctt gac aca cgg tac ctg gag 288  
 782 Met Ala Gln Trp Asn Gln Leu Gln Leu Asp Thr Arg Tyr Leu Glu  
 783 1 5 10 15  
 785 cag ctc cat cag ctc tac agt gac agc ttc cca atg gag ctg cgg cag 336  
 786 Gln Leu His Gln Leu Tyr Ser Asp Ser Phe Pro Met Glu Leu Arg Gln  
 787 20 25 30  
 789 ttt ctg gcc cct tgg att gag agt caa gat tgg gca tat gcg gcc agc 384  
 790 Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser  
 791 35 40 45  
 793 aaa gaa tca cat gcc act ttg gtg ttt cat aat ctc ctg gga gag att 432  
 794 Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile  
 795 50 55 60  
 797 gac cag cag tat agc cgc ttc ctg caa gag tcg aat gtt ctc tat cag 480  
 798 Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln  
 799 65 70 75 80  
 801 cac aat cta cga aga atc aag cag ttt ctt cag agc agg tat ctt gag 528  
 802 His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu  
 803 85 90 95  
 805 aag cca atg gag att gcc cgg att gtg gcc cgg tgc ctg tgg gaa gaa 576  
 806 Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu  
 807 100 105 110  
 809 tca cgc ctt cta cag act gca gcc act gcg gcc cag caa ggg ggc cag 624  
 810 Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln  
 811 115 120 125  
 813 gcc aac cac ccc aca gca gcc gtg gtg acg gag aag cag cag atg ctg 672  
 814 Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu  
 815 130 135 140  
 817 gag cag cac ctt cag gat gtc cgg aag aga gtg cag gat cta gaa cag 720  
 818 Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln  
 819 145 150 155 160  
 821 aaa atg aaa gtg gta gag aat ctc cag gat gac ttt gat ttc aac tat 768  
 822 Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr  
 823 165 170 175  
 825 aaa acc ctc aag agt caa gga gac atg caa gat ctg aat gga aac aac 816  
 826 Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn  
 827 180 185 190  
 829 cag tca gtg acc agg cag aag atg cag cag ctg gaa cag atg ctc act 864  
 830 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr  
 831 195 200 205  
 833 gcg ctg gac cag atg cgg aga agc atc gtg agt gag ctg gcg ggg ctt 912  
 834 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu  
 835 210 215 220  
 837 ttg tca gcg atg gag tac gtg cag aaa act ctc acg gac gag gag ctg 960  
 838 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Asp Glu Glu Leu

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Input Set : A:\PTO.TS..txt  
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839	225	230	235	240	
841	gct gac tgg aag agg cgg caa cag att gcc tgc att gga ggc ccg ccc				1008
842	Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro				
843	245	250	255		
845	aac atc tgc cta gat cgg cta gaa aac tgg ata acg tca tta gca gaa				1056
846	Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu				
847	260	265	270		
849	tct caa ctt cag acc cgt caa caa att aag aaa ctg gag gag ttg cag				1104
850	Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln				
851	275	280	285		
853	caa aaa gtt tcc tac aaa ggg gac ccc att gta cag cac cgg ccg atg				1152
854	Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met				
855	290	295	300		
857	ctg gag gag aga atc gtg gag ctg ttt aga aac tta atg aaa agt gcc				1200
858	Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala				
859	305	310	315	320	
861	ttt gtg gtg gag cgg cag ccc tgc atg ccc atg cat cct gac cgg ccc				1248
862	Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro				
863	325	330	335		
865	ctc gtc atc aag acc ggc gtc cag ttc act act aaa gtc agg ttg ctg				1296
866	Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu				
867	340	345	350		
869	gtc aaa ttc cct gag ttg aat tat cag ctt aaa att aaa gtg tgc att				1344
870	Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile				
871	355	360	365		
873	gac aaa gac tct ggg gac gtt gca gct ctc aga gga tcc cgg aaa ttt				1392
874	Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe				
875	370	375	380		
877	aac att ctg ggc aca aac aca aaa gtg atg aac atg gaa gaa tcc aac				1440
878	Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn				
879	385	390	395	400	
881	aac ggc agc ctc tct gca gaa ttc aaa cac ttg acc ctg agg gag cag				1488
882	Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln				
883	405	410	415		
885	aga tgt ggg aat ggg ggc cga gcc aat tgt gat gct tcc ctg att gtg				1536
886	Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val				
887	420	425	430		
889	act gag gag ctg cac ctg atc acc ttt gag acc gag gtg tat cac caa				1584
890	Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln				
891	435	440	445		
893	ggc ctc aag att gac cta gag acc cac tcc ttg cca gtt gtg gtg atc				1632
894	Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile				
895	450	455	460		
897	tcc aac atc tgt cag atg cca aat gcc tgg gcg tcc atc ctg tgg tac				1680
898	Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr				
899	465	470	475	480	
901	aac atg ctg acc aac aat ccc aag aat gta aac ttt ttt acc aag ccc				1728
902	Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro				
903	485	490	495		

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Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

905	cca	att	gga	acc	tgg	gat	caa	gtg	gcc	gag	gtc	ctg	agc	tgg	cag	ttc	1776	
906	Pro	Ile	Gly	Thr	Trp	Asp	Gln	Val	Ala	Glu	Val	Leu	Ser	Trp	Gln	Phe		
907							500				505					510		
909	tcc	tcc	acc	acc	aag	cga	gga	ctg	agc	atc	gag	cag	ctg	act	aca	ctg	1824	
910	Ser	Ser	Thr	Thr	Lys	Arg	Gly	Leu	Ser	Ile	Glu	Gln	Leu	Thr	Thr	Leu		
911							515				520					525		
913	gca	gag	aaa	ctc	ttg	gga	cct	ggt	gtg	aat	tat	tca	ggg	tgt	cag	atc	1872	
914	Ala	Glu	Lys	Leu	Leu	Gly	Pro	Gly	Val	Asn	Tyr	Ser	Gly	Cys	Gln	Ile		
915							530				535					540		
917	aca	tgg	gct	aaa	ttt	tgc	aaa	gaa	aac	atg	gct	ggc	aag	ggc	ttc	tcc	1920	
918	Thr	Trp	Ala	Lys	Phe	Cys	Lys	Glu	Asn	Met	Ala	Gly	Lys	Gly	Phe	Ser		
919	545						550				555					560		
921	tcc	tgg	gtc	tgg	ctg	gac	aat	atc	att	gac	ctt	gtg	aaa	aag	tac	atc	1968	
922	Phe	Trp	Val	Trp	Leu	Asp	Asn	Ile	Ile	Asp	Leu	Val	Lys	Lys	Tyr	Ile		
923							565				570					575		
925	ctg	gcc	ctt	tgg	aac	gaa	ggg	tac	atc	atg	ggc	ttt	atc	agt	aag	gag	2016	
926	Leu	Ala	Leu	Trp	Asn	Glu	Gly	Tyr	Ile	Met	Gly	Phe	Ile	Ser	Lys	Glu		
927							580				585					590		
929	cgg	gag	cgg	gcc	atc	ttg	agc	act	aag	cct	cca	ggc	acc	ttc	ctg	cta	2064	
930	Arg	Glu	Arg	Ala	Ile	Leu	Ser	Thr	Lys	Pro	Pro	Gly	Thr	Phe	Leu	Leu		
931							595				600					605		
933	aga	tcc	agt	gaa	agc	agc	aaa	gaa	gga	ggc	gtc	act	ttc	act	tgg	gtg	2112	
934	Arg	Phe	Ser	Glu	Ser	Ser	Lys	Glu	Gly	Gly	Val	Thr	Phe	Thr	Trp	Val		
935							610				615					620		
937	gag	aag	gac	atc	agc	ggt	aag	acc	cag	atc	cag	tcc	gtg	gaa	cca	tac	2160	
938	Glu	Lys	Asp	Ile	Ser	Gly	Lys	Thr	Gln	Ile	Gln	Ser	Val	Glu	Pro	Tyr		
939	625						630				635					640		
941	aca	aag	cag	cag	ctg	aac	aac	atg	tca	ttt	gct	gaa	atc	atc	atg	ggc	2208	
942	Thr	Lys	Gln	Gln	Leu	Asn	Asn	Met	Ser	Phe	Ala	Glu	Ile	Ile	Met	Gly		
943							645				650					655		
945	tat	aag	atc	atc	atg	gat	gct	acc	aat	atc	ctg	gtg	tct	cca	ctg	gtc	tat	2256
946	Tyr	Lys	Ile	Met	Asp	Ala	Thr	Asn	Ile	Leu	Val	Ser	Pro	Leu	Val	Tyr		
947							660				665					670		
949	ctc	tat	cct	gac	att	ccc	aag	gag	gag	gca	ttc	gga	aag	tat	tgt	cgg	2304	
950	Leu	Tyr	Pro	Asp	Ile	Pro	Lys	Glu	Glu	Ala	Phe	Gly	Lys	Tyr	Cys	Arg		
951							675				680					685		
953	cca	gag	agc	cag	gag	cat	cct	gaa	gct	gac	cca	ggt	agc	gct	gcc	cca	2352	
954	Pro	Glu	Ser	Gln	Glu	His	Pro	Glu	Ala	Asp	Pro	Gly	Ser	Ala	Ala	Pro		
955							690				695					700		
957	tac	ctg	aag	acc	aag	ttt	atc	tgt	gtg	aca	cca	acg	acc	tgc	agc	aat	2400	
958	Tyr	Leu	Lys	Thr	Lys	Phe	Ile	Cys	Val	Thr	Pro	Thr	Thr	Cys	Ser	Asn		
959	705						710				715					720		
961	acc	att	gac	ctg	ccg	atg	tcc	ccc	cgc	act	tta	gat	tca	ttg	atg	cag	2448	
962	Thr	Ile	Asp	Leu	Pro	Met	Ser	Pro	Arg	Thr	Leu	Asp	Ser	Leu	Met	Gln		
963							725				730					735		
965	ttt	gga	aat	aat	ggt	gaa	ggt	gct	gaa	ccc	tca	gca	gga	ggg	cag	ttt	2496	
966	Phe	Gly	Asn	Asn	Gly	Glu	Gly	Ala	Glu	Pro	Ser	Ala	Gly	Gly	Gln	Phe		
967							740				745					750		
969	gag	tcc	ctc	acc	ttt	gac	atg	gag	ttg	acc	tgc	gag	tgc	gct	acc	tcc	2544	

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006

TIME: 14:09:12

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

970 Glu Ser Leu Thr Phe Asp Met Glu Leu Thr Ser Glu Cys Ala Thr Ser  
 971 755 760 765  
 973 ccc atg tga ggagctgaga acggaagctg cagaaagata cgactgaggc 2593  
 974 Pro Met  
 975 770  
 977 gcctacctgc attctgccac ccctcacaca gccaaacccc agatcatctg aaactactaa 2653  
 979 ctttgtggtt ccagatttt ttaatctcc tacttctgtc atctttgagc aatctggca 2713  
 981 cttttaaaaa tagagaaatg agtgaatgtt ggtgatctgc ttttatctaa atgcaaataa 2773  
 983 ggtatgtttc tctgagaccc atgatcaggg gatgtggcgg ggggtggcta gaggagaaa 2833  
 985 aaggaaatgt cttgtgtgtt tttgttcccc tgccttc ttcagcagc tttttgttat 2893  
 987 tgggtgtgtt gttcttagac aagtgcctcc tggtcctgc ggcatttc tgcctgtttc 2953  
 989 tggtaagcaaa tgccacaggc cacctatagc tacatactcc tggcattgca cttttaacc 3013  
 991 ttgctgacat ccaaataagaa gataggacta tctaagccct aggtttctt ttaaattaag 3073  
 993 aaataataac aattaaaggc caaaaaacac tggatcagca tagccttct gtatttaaga 3133  
 995 aacttaagca gcccggcatg gttggctcaag cctgtatcc cagcactttg ggaggccgag 3193  
 997 gcccggatcata aggtcaggag atcaagacca tcctggctaa cacggtaaa ccccgctct 3253  
 999 actaaaagta caaaaaattt gttgggtgtt gttggggcgc cctgtatc cagctactcg 3313  
 1001 ggaggctgag gcaggagaat cgcttgcacc tgagaggcgg aggttgcagt gagccaaaat 3373  
 1003 tgcaccactg cacactgcac tccatcctgg ggcacagtct gagactctgt ctcaaaaaaaa 3433  
 1005 aaaaaaaaaa aaagaaaactt cagttAACAG cctccttgg gctttaagca ttcaagttcc 3493  
 1007 ttcaggctgg taatttatat aatccctgaa acgggcttca ggtcaaaaaa ttaagacatc 3553  
 1009 tgaagctgca acctggcctt tgggtgtt gaa ataggaaggt ttaaggagaa tctaaggatt 3613  
 1011 ttagactttt ttttataat agacttattt tccttgcattt tttttttttt tttttttttt 3673  
 1013 taaggctggg cagagggtgc ttacaacccctt gactccctt cttttttttt tttttttttt 3733  
 1015 gtttcagagg ctaggttgcattt tctgtgggtt cttttttttt tttttttttt 3793  
 1017 ggcttccttc ctggcccccacc ctccccgaccc cttttttttt tttttttttt 3853  
 1019 tccttgcgtt tctaaaggccctt cttttttttt tttttttttt tttttttttt 3913  
 1021 catggaaagaa gaggggggaga gatgttacagg ttggacatga tttttttttt tttttttttt 3973  
 1023 cgacgtgtct gtttgcgttcc acggaaatatg gttttttttt tttttttttt 4033  
 1025 tggacttgcattt aatggcgatc tttttttttt tttttttttt 4093  
 1027 gagttctggcc tctgtatgagg gtttgcattt gttttttttt tttttttttt 4153  
 1029 tgctggggcc ccacagggtt gttttttttt tttttttttt 4213  
 1031 ctggcttagct cttttttttt tttttttttt 4273  
 1033 tctgtactcg aggcatggcc gttttttttt tttttttttt 4333  
 1035 agtttctgtt gttttttttt tttttttttt 4393  
 1037 cgaccttctc taagatgaac gttttttttt tttttttttt 4453  
 1039 gtcatgcaga gttttttttt tttttttttt 4513  
 1041 aaacagaata tttttttttt tttttttttt 4573  
 1043 tagggcgagg gttttttttt tttttttttt 4633  
 1045 catgtatctg gttttttttt tttttttttt 4693  
 1047 tggcccaattt aagaacagggtt gttttttttt tttttttttt 4753  
 1049 catccccaggcc cttttttttt tttttttttt 4813  
 1051 aagctgtgtt cttttttttt tttttttttt 4873  
 1053 atattattgtt gttttttttt tttttttttt 4933  
 1055 ctacttttaac tttttttttt tttttttttt 4978  
 1058 <210> SEQ ID NO: 20  
 1059 <211> LENGTH: 3631  
 1060 <212> TYPE: mRNA  
 1061 <213> ORGANISM: Homo sapiens

1060  $\times$  212 TYPE mRNA

1060 <212> TYPE: MNA

1061 <213> ORGANISM: homo sapiens

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006  
TIME: 14:09:12

Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

1063 <220> FEATURE:  
1064 <221> NAME/KEY: CDS  
1065 <222> LOCATION: (549)..(2147)  
1067 <400> SEQUENCE: 20  
1068 gcggccgtc cagagatgg aatccgcctg ccgggcttgg cgaaggagaa gggaggaggc 60  
1070 aggagcgagg agggaggagg gccaaggcg ggcaggaagg cttaggctcg ggcgtccgt 120  
1072 ccgcgcgcg cgaagatcgc acggcccgat cgaggggcga ccgggtcggg gccgctgcac 180  
1074 gccaaggcg aaggccgatt cgggcccac ttccgcggg cggctcgcg cggccacccg 240  
1076 ctccgcgcg aggctggag gatgcgttcc ctggggtccg gacttatgaa aatatgcac 300  
1078 agttaatac tgtcttgaa ttcatgagat ggaagcatag gtcaagctg ttggagaaa 360  
1080 atcagaagta cagtttatac tagccacatc ttggaggagt cgtaaagaaag cagtgggagt 420  
1082 tgaagtcatt gtcaagtgc tgcatctt tacaagaaaa tctcactgaa tgatagtcat 480  
1084 ttaaatttgtt gaagtagcaa gaccaattat taaaggtgac agtacacagg aaacattaca 540  
1086 attgaaca atg cct cag cta tac att tac atc aga tta ttg gga gcc tat 590  
1087 Met Pro Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala Tyr  
1088 1 5 10  
1090 ttg ttc atc att tct cgt gtt caa gga cag aat ctg gat agt atg ctt 638  
1091 Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met Leu  
1092 15 20 25 30  
1094 cat ggc act ggg atg aaa tca gac tcc gac cag aaa aag tca gaa aat 686  
1095 His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Ser Glu Asn  
1096 35 40 45  
1098 gga gta acc tta gca cca gag gat acc ttg cct ttt tta aag tgc tat 734  
1099 Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys Tyr  
1100 50 55 60  
1102 tgc tca ggg cac tgt cca gat gat gct att aat aac aca tgc ata act 782  
1103 Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile Thr  
1104 65 70 75  
1106 aat gga cat tgc ttt gcc atc ata gaa gaa gat gac cag gga gaa acc 830  
1107 Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu Thr  
1108 80 85 90  
1110 aca tta gct tca ggg tgt atg aaa tat gaa gga tct gat ttt cag tgc 878  
1111 Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys  
1112 95 100 105 110  
1114 aaa gat tct cca aaa gcc cag cta cgc cgg aca ata gaa tgt tgt cgg 926  
1115 Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg  
1116 115 120 125  
1118 acc aat tta tgt aac cag tat ttg caa ccc aca ctg ccc cct gtt gtc 974  
1119 Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val Val  
1120 130 135 140  
1122 ata ggt ccg ttt ttt gat ggc agc att cga tgg ctg gtt ttg ctc att 1022  
1123 Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Ile  
1124 145 150 155  
1126 tct atg gct gtc tgc ata att gct atg atc atc ttc tcc agc tgc ttt 1070  
1127 Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe  
1128 160 165 170  
1130 tgt tac aaa cat tat tgc aag agc atc tca agc aga cgt cgt tac aat 1118  
1131 Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn  
1132 175 180 185 190

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006  
TIME: 14:09:12

Input Set : A:\PTO.TS..txt  
Output Set: N:\CRF4\03212006\J571511.raw

1134	cgt gat ttg gaa cag gat gaa gca ttt att cca gtt gga gaa tca cta	1166
1135	Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser Leu	
1136	195 200 205	
1138	aaa gac ctt att gac cag tca caa agt tct ggt agt ggg tct gga cta	1214
1139	Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu	
1140	210 215 220	
1142	cct tta ttg gtt cag cga act att gcc aaa cag att cag atg gtc cgg	1262
1143	Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg	
1144	225 230 235	
1146	caa gtt ggt aaa ggc cga tat gga gaa gta tgg atg ggc aaa tgg cgt	1310
1147	Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg	
1148	240 245 250	
1150	ggc gaa aaa gtg gcg gtg aaa gta ttc ttt acc act gaa gaa gcc agc	1358
1151	Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser	
1152	255 260 265 270	
1154	tgg ttt cga gaa aca gaa atc tac caa act gtg cta atg cgc cat gaa	1406
1155	Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu	
1156	275 280 285	
1158	aac ata ctt ggt ttc ata gcg gca gac att aaa ggt aca ggt tcc tgg	1454
1159	Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp	
1160	290 295 300	
1162	act cag ctc tat ttg att act gat tac cat gaa aat gga tct ctc tat	1502
1163	Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr	
1164	305 310 315	
1166	gac ttc ctg aaa tgt gct aca ctg gac acc aga gcc ctg ctt aaa ttg	1550
1167	Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu	
1168	320 325 330	
1170	gct tat tca gct gcc tgt ggt ctg tgc cac ctg cac aca gaa att tat	1598
1171	Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr	
1172	335 340 345 350	
1174	ggc acc caa gga aag ccc gca att gct cat cga gac cta aag agc aaa	1646
1175	Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys	
1176	355 360 365	
1178	aac atc ctc atc aag aaa aat ggg agt tgc tgc att gct gac ctg ggc	1694
1179	Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly	
1180	370 375 380	
1182	ctt gct gtt aaa ttc aac agt gac aca aat gaa gtt gat gtg ccc ttg	1742
1183	Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu	
1184	385 390 395	
1186	aat acc agg gtg ggc acc aaa cgc tac atg gct ccc gaa gtg ctg gac	1790
1187	Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp	
1188	400 405 410	
1190	gaa agc ctg aac aaa aac cac ttc cag ccc tac atc atg gct gac atc	1838
1191	Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile	
1192	415 420 425 430	
1194	tac agc ttc ggc cta atc att tgg gag atg gct cgt cgt tgt atc aca	1886
1195	Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr	
1196	435 440 445	
1198	gga ggg atc gtg gaa tac caa ttg cca tat tac aac atg gta ccg	1934

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006

TIME: 14:09:12

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

1199	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	
1200				450				455				455		460			
1202	agt	gat	ccg	tca	tac	gaa	gat	atg	cgt	gag	gtt	gtg	tgt	gtc	aaa	cgt	1982
1203	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Val	Val	Cys	Val	Lys	Arg	
1204			465					470				475					
1206	ttg	cg	cca	att	gtg	tct	aat	cgg	tgg	aac	agt	gat	gaa	tgt	cta	cga	2030
1207	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg	Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	
1208			480				485				490						
1210	gca	gtt	ttg	aag	cta	atg	tca	gaa	tgc	tgg	gcc	cac	aat	cca	gcc	tcc	2078
1211	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	
1212	495				500				505				510				
1214	aga	ctc	aca	gca	ttg	aga	att	aag	aag	acg	ctt	gcc	aag	atg	gtt	gaa	2126
1215	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	
1216					515			520			525						
1218	tcc	caa	gat	gta	aaa	atc	tga	ttgttaaacc	atcgaggag	aaactctaga							2177
1219	Ser	Gln	Asp	Val	Lys	Ile											
1220				530													
1222	ctgcaagaac	tggttttacc	catggcatgg	gtggaaattag	agtggaaataa	ggatgttaac	2237										
1224	ttgggttctca	gactcttct	tcactacgtg	ttcacaggct	gctaataattta	aacctttcag	2297										
1226	tactcttatt	aggatacaag	ctggggaaactt	ctaaacactt	cattctttat	atatggacag	2357										
1228	ctttatTTta	aatgtggTTt	ttgatgcTTt	tttttaagtg	ggttttatg	aactgcatca	2417										
1230	agacttcaat	cctgattagt	gtctccagtc	aagctctggg	tactgaattt	cctgttcata	2477										
1232	aaacgggtct	ttctgtgaaa	gccttaagaa	gataaatgag	cgcagcagag	atggagaaat	2537										
1234	agactttgcc	ttttacctga	gacattcagt	tcgtttgtat	tctaccttt	taaaacagcc	2597										
1236	tatagatgt	gatgtgttt	ggatactgt	tattttatga	tagtttgcc	tgtgtccctta	2657										
1238	gtgatgtgt	tgtgtctcca	tgcacatgca	cggccggatt	cctctgtcgc	catttgaatt	2717										
1240	agaagaaaat	aatttatatg	catgcacagg	aagatattgg	tggccgtgg	ttttgtgctt	2777										
1242	taaaaatgca	atatctgacc	aagattcgcc	aatctcatac	aagccattta	ctttgcaagt	2837										
1244	gagatagctt	ccccaccagc	tttattttt	aacatgaaag	ctgatgcca	ggccaaaaga	2897										
1246	agtttaaagc	atctgttaat	ttggactgtt	ttccttcaac	caccattttt	tttgggttta	2957										
1248	ttatTTTgt	cacggaaagc	atcctctcca	aagtggagc	ttctattgcc	atgaaccatg	3017										
1250	cttacaaaga	aagcacttct	tattgaagtg	aattctgca	tttgatagca	atgttaagtgc	3077										
1252	ctataaccat	gttcttatatt	cttatttctc	agtaacttt	aaaagggaag	ttatttatat	3137										
1254	tttgggtata	atgtgcttta	tttgcaaaatc	acccactcct	ttacaaccat	actttatata	3197										
1256	tgtacataca	ttcatactgt	agaaaaccagc	tcatgtgtac	ctcatatccc	atcccttaaga	3257										
1258	gaagaaaatgt	tataaagtag	aactaaatat	aaattttcag	aattaatgca	ttcaaagtagaa	3317										
1260	tatataaaat	ccaggacttt	gttaacttca	ggtaaaaaact	tcattaggt	aatatcatct	3377										
1262	caatTTTTtc	aaatgaaagg	attctctaatt	tagaaattta	tatgtcagag	ctgttataaaa	3437										
1264	tttatcaact	gtcaaataatg	ttctggacag	ctaaatcatt	tgagattttt	ggttttttga	3497										
1266	tttctattcc	ctaaacttgt	aagacaatga	aaaatcaggc	agaaatattt	agtatctagt	3557										
1268	cagtatctgt	agctacactg	tataactgtt	cttcaataaa	atggttcata	ttttatagaa	3617										
1270	aaaaaaaaaa	aaaa					3631										

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/571,511

DATE: 03/21/2006

TIME: 14:09:13

Input Set : A:\PTO.TS..txt

Output Set: N:\CRF4\03212006\J571511.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:26 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:1  
L:175 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:2  
L:331 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:3  
L:456 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4  
L:765 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:19  
L:1060 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:20